AMENDMENTS TO THE SPECIFICATION

Please replace the abstract with the following amended abstract:

~~The present invention relates to m~~Methods of isolating cells or generating cell lines comprising the step of exposing the cells to ~~using~~ signaling probes that produce a signal upon hybridization to a target sequence, as well as ~~. Other methods that utilize the signaling probe include~~ methods of quantifying the level of ~~RNA~~ expression of an RNA of interest, methods for identifying genetic recombinational events in living cells and methods of generating a transgenic animal using the isolated cells. Methods for isolating a plurality of cells encoding a plurality of different RNAs associated with a same nucleic acid tag sequence, comprising the step of exposing the cells to a same signaling probe that produces a detectable signal upon hybridization to the same nucleic acid tag sequence, are also provided. ~~The invention also provides protease probes.~~ Signaling probes and protease probes that form stem-loop structures, three-arm junction structures, and dumbbell structures ~~are provided~~ may be used in the above methods.

Please replace the paragraph on p. 1, after the title, with the following amended paragraph:

This application is a national stage entry of International Application No. PCT/US2005/005080, filed February 17, 2005, which claims priority from United States ~~provisional application number~~ Provisional Application No. 60/546,075, filed February 18, 2004~~, the disclosure of which is incorporated in its entirety by~~

~~reference herein~~. The disclosures of all of the aforementioned priority applications are incorporated by reference in their entirety herein.

Please replace paragraphs [0032]-[0034] with the following amended paragraphs:

[0032] Figure 8 shows the sequence and predicted native conformation of fluorescent probe FP1. The FP1 sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. Panel A shows the predicted structure of the sequence using DNA folding programs according to *Nucleic Acids Res.* 31: 3429-3431 (2003). Panel B shows predicted self dimerization of the FP1 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. In both Panels A and B, the flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

[0033] Figure 9 shows the sequence and predicted native conformation of fluorescent probe FP2. The sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. Panel A shows the predicted structure of the sequence using DNA folding programs according to *Nucleic Acids Res.* 31: 3429-3431 (2003). It is likely that all or part of the shaded region form Watson-Crick basepairs, thereby forming a three-arm junction. Panel B shows predicted self dimerization of the FP2 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website

~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. In both Panels A and B, the flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

[0034] Figure 10 shows the sequence and predicted native conformation of fluorescent probe FP3. The FP3 sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. The figure shows predicted self dimerization of the FP3 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. The flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

Please replace paragraphs [0037] and [0038] with the following amended paragraphs:

[0037] Figure 14 shows the sequence and predicted native conformation of fluorescent probe FP7. The FP7 sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. The predicted self dimerization of the FP7 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~ is shown. The flanking bases

are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

[0038] Figure 15 shows the sequence and predicted native conformation of fluorescent probe FP8. The FP8 sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. Panel A shows the predicted structure of the sequence using DNA folding programs according to *Nucleic Acids Res.* 31: 3429-3431 (2003). Panel B shows predicted self dimerization of the FP1 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. In both Panels A and B, the flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

Please replace paragraph [0041] with the following amended paragraph:

[0041] Figures 22 through 24 show the sequence and predicted native conformation of fluorescent probes FP15 to 17, respectively. The sequences comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. Panel A shows the predicted structure of the sequence using DNA folding programs according to *Nucleic Acids Res.* 31: 3429-3431 (2003). Panel B shows predicted self dimerization of the FP15 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. In both Panels A and B, the

flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

Please replace paragraph [0041] with the following amended paragraph:

[0062] Figure 41 shows the sequence and predicted native conformation of fluorescent probe FP18. The sequence comprises bases which are designed to be complementary to the target sequence and additional flanking bases. The flanking bases are underlined. Panel A shows the predicted structure of the sequence using DNA folding programs according to *Nucleic Acids Res.* 31: 3429-3431 (2003). Panel B shows predicted self dimerization of the FP2 sequence according to the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~. In both Panels A and B, the flanking bases are shaded in grey, white and black ovals indicate fluorophore and quencher moieties, respectively.

Please replace paragraph [0041] with the following amended paragraph:

[0122] DNA or RNA folding programs are available in the art to predict the conformation of a given nucleic acid or modified nucleic acid. Such folding programs include but are not limited to the programs described in *Nucleic Acids Res.* 31: 3429-3431 (2003) and the oligoanalyzer 3.0 software available at the Integrated DNA Technologies SciTools website ~~http://biotools.idtdna.com/analyzer/oligocalc.asp~~; hereby incorporated by reference. Such folding programs often predict a number of energetically more

favorable structures. In other embodiments, the invention encompasses the energetically more favorable structures of probes FP1-18 (Figures 8-24 and 41) that are predicted by folding programs. If the energy of the conformation is measured by free energy, the lower free energy value (negative) indicates that the conformation is more energetically favorable.